

SEQUENCE LISTING

<110> DUSCH, Nicole
THOMAS, Hermann
THIERBACH, Georg

<120> PROCESS FOR THE FERMENTATIVE PREPARATION OF D-PANTOTHENOIC
ACID USING CORYNEFORM BACTERIA

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<151> 2000-09-30

<150> DE 10117085.8

<151> 2001-04-06

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<170> PatentIn version 3.1

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<213> Corynebacterium glutamicum

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Ala Glu Ser Leu Ile Thr Gly Glu Leu Ala Val Cys Ala Ala Ser Cys

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Gly Pro Gly Asn Thr His Leu Ile Gln Gly Leu Tyr Asp Ser His Arg

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Asn Gly Ala Lys Val Leu Ala Ile Ala Ser His Ile Pro Ser Ala Gln
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 Ile Gly Ser Thr Phe Phe Gln Glu Thr His Pro Glu Ile Leu Phe Lys
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gaa tgc tct ggt tac tgc gag atg gtg aat ggt ggt gag cag ggt gaa
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 Glu Cys Ser Gly Tyr Cys Glu Met Val Asn Gly Gly Glu Gln Gly Glu
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cgc att ttg cat cac gcg att cag tcc acc atg gcg ggt aaa ggt gtg
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 Arg Ile Leu His His Ala Ile Gln Ser Thr Met Ala Gly Lys Gly Val
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 Gly Thr Tyr Ser Asn Ser Thr Ile Ser Ser Gly Thr Pro Val Val Phe
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ccg gat cct act gag gct gca gcg ctg gtg gag gcg att aac aac gct
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 Pro Asp Pro Thr Glu Ala Ala Ala Leu Val Glu Ala Ile Asn Asn Ala
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 Lys Ser Val Thr Leu Phe Cys Gly Ala Gly Val Lys Asn Ala Arg Ala
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cag gtg ttg gag ttg gcg gag aag att aaa tca ccg atc ggg cat gcg
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Gln Val Leu Glu Leu Ala Glu Lys Ile Lys Ser Pro Ile Gly His Ala

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225

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ctg ggt ggt aag cag tac atc cag cat gag aat ccg ttt gag gtc ggc
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Leu Gly Gly Lys Gln Tyr Ile Gln His Glu Asn Pro Phe Glu Val Gly

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atg tct ggc ctg ctt ggt tac ggc gcc tgc gtg gat gcg tcc aat gag
1121

Met Ser Gly Leu Leu Gly Tyr Gly Ala Cys Val Asp Ala Ser Asn Glu

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255

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265

gcg gat ctg ctg att cta ttg ggt acg gat ttc cct tat tct gat ttc
1169

Ala Asp Leu Leu Ile Leu Leu Gly Thr Asp Phe Pro Tyr Ser Asp Phe

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275

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1217

Leu Pro Lys Asp Asn Val Ala Gln Val Asp Ile Asn Gly Ala His Ile

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1265

Gly Arg Arg Thr Thr Val Lys Tyr Pro Val Thr Gly Asp Val Ala Ala

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Thr Ile Glu Asn Ile Leu Pro His Val Lys Glu Lys Thr Asp Arg Ser

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Phe Leu Asp Arg Met Leu Lys Ala His Glu Arg Lys Leu Ser Ser Val

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Ala Val Val Phe Asn Asn Ser Ser Leu Gly Met Val Lys Leu Glu Met

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Leu Val Glu Gly Gln Pro Glu Phe Gly Thr Asp His Glu Glu Val Asn

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1841

Phe Ala Glu Ile Ala Ala Ala Ala Gly Ile Lys Ser Val Arg Ile Thr

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1937

Gly Pro Val Leu Ile Asp Ile Val Thr Asp Pro Asn Ala Leu Ser Ile

525

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535

cca cca acc atc acg tgg gaa cag gtc atg gga ttc agc aag gcg gcc
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Pro Pro Thr Ile Thr Trp Glu Gln Val Met Gly Phe Ser Lys Ala Ala

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Thr Arg Thr Val Phe Gly Gly Gly Val Gly Ala Met Ile Asp Leu Ala

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560

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Arg Ser Asn Ile Arg Asn Ile Pro Thr Pro

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Glu Leu Ala Val Cys Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu
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Glu Thr His Pro Glu Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu
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Gln Ser Thr Met Ala Gly Lys Gly Val Ser Val Val Val Ile Pro Gly
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Asp Ile Ala Lys Glu Asp Ala Gly Asp Gly Thr Tyr Ser Asn Ser Thr
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Ile Ser Ser Gly Thr Pro Val Val Phe Pro Asp Pro Thr Glu Ala Ala
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Gly Ala Gly Val Lys Asn Ala Arg Ala Gln Val Leu Glu Leu Ala Glu
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225 230 235 240

Gln His Glu Asn Pro Phe Glu Val Gly Met Ser Gly Leu Leu Gly Tyr
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Gly Thr Asp Phe Pro Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala
275 280 285

Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys
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305 310 315 320

His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys
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Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn
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Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu
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Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met
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Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg
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Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu
465 470 475 480

Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala
485 490 495

Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu
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515 520 525

Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu
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780

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831

Met Ala His Ser Tyr Ala Glu Gln Leu Ile

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879

Asp Thr Leu Glu Ala Gln Gly Val Lys Arg Ile Tyr Gly Leu Val Gly

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gac agc ctt aat ccg atc gtg gat gct gtc cgc caa tca gat att gag
927

Asp Ser Leu Asn Pro Ile Val Asp Ala Val Arg Gln Ser Asp Ile Glu

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975

Trp Val His Val Arg Asn Glu Glu Ala Ala Ala Phe Ala Ala Gly Ala

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1023

Glu Ser Leu Ile Thr Gly Glu Leu Ala Val Cys Ala Ala Ser Cys Gly

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1071

Pro Gly Asn Thr His Leu Ile Gln Gly Leu Tyr Asp Ser His Arg Asn

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1119

Gly Ala Lys Val Leu Ala Ile Ala Ser His Ile Pro Ser Ala Gln Ile

95

100

105

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1167

Gly Ser Thr Phe Phe Gln Glu Thr His Pro Glu Ile Leu Phe Lys Glu

110

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1215

Cys Ser Gly Tyr Cys Glu Met Val Asn Gly Gly Glu Gln Gly Glu Arg

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1263

Ile Leu His His Ala Ile Gln Ser Thr Met Ala Gly Lys Gly Val Ser

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145

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1311

Val Val Val Ile Pro Gly Asp Ile Ala Lys Glu Asp Ala Gly Asp Gly

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160

165

170

act tat tcc aat tcc act att tct tct ggc act cct gtg gtg ttc ccg
1359

Thr Tyr Ser Asn Ser Thr Ile Ser Ser Gly Thr Pro Val Val Phe Pro

175

180

185

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1407

Asp Pro Thr Glu Ala Ala Ala Leu Val Glu Ala Ile Asn Asn Ala Lys

190

195

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1455
Ser Val Thr Leu Phe Cys Gly Ala Gly Val Lys Asn Ala Arg Ala Gln

205

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gtg ttg gag ttg gcg gag aag att aaa tca ccg atc ggg cat gcg ctg
1503

Val Leu Glu Leu Ala Glu Lys Ile Lys Ser Pro Ile Gly His Ala Leu

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225

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ggg ggt aag cag tac atc cag cat gag aat ccg ttt gag gtc ggc atg
1551

Gly Gly Lys Gln Tyr Ile Gln His Glu Asn Pro Phe Glu Val Gly Met

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tct ggc ctg ctt ggt tac ggc gcc tgc gtg gat gcg tcc aat gag gcg
1599

Ser Gly Leu Leu Gly Tyr Gly Ala Cys Val Asp Ala Ser Asn Glu Ala

255

260

265

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1647

Asp Leu Leu Ile Leu Leu Gly Thr Asp Phe Pro Tyr Ser Asp Phe Leu

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275

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1695

Pro Lys Asp Asn Val Ala Gln Val Asp Ile Asn Gly Ala His Ile Gly

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290

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1743

Arg Arg Thr Thr Val Lys Tyr Pro Val Thr Gly Asp Val Ala Ala Thr

300

305

310

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1791

Ile Glu Asn Ile Leu Pro His Val Lys Glu Lys Thr Asp Arg Ser Phe

315

320

325

330

ctt gat cgg atg ctc aag gca cac gag cgt aag ttg agc tcg gtg gta
1839

Leu Asp Arg Met Leu Lys Ala His Glu Arg Lys Leu Ser Ser Val Val

335

340

345

gag acg tac aca cat aac gtc gag aag cat gtg cct att cac cct gaa
1887

Glu Thr Tyr Thr His Asn Val Glu Lys His Val Pro Ile His Pro Glu

350

355

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1935

Tyr Val Ala Ser Ile Leu Asn Glu Leu Ala Asp Lys Asp Ala Val Phe

365

370

375

act gtg gat acc ggc atg tgc aat gtg tgg cat gcg agg tac atc gag
1983

Thr Val Asp Thr Gly Met Cys Asn Val Trp His Ala Arg Tyr Ile Glu

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385

390

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2031

Asn Pro Glu Gly Thr Arg Asp Phe Val Gly Ser Phe Arg His Gly Thr

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2079

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420

425

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2127

Asn Arg Gln Val Ile Ala Met Cys Gly Asp Gly Gly Leu Gly Met Leu

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2175
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445

450

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2223
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465

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2271
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475

480

485

490

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2319
Ala Glu Ile Ala Ala Ala Ala Gly Ile Lys Ser Val Arg Ile Thr Asp

495

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2367
Pro Lys Lys Val Arg Glu Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly

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515

520

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2415
Pro Val Leu Ile Asp Ile Val Thr Asp Pro Asn Ala Leu Ser Ile Pro

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50 55 60

Glu Leu Ala Val Cys Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu
65 70 75 80

Ile Gln Gly Leu Tyr Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala
85 90 95

Ile Ala Ser His Ile Pro Ser Ala Gln Ile Gly Ser Thr Phe Phe Gln
100 105 110

Glu Thr His Pro Glu Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu
115 120 125

Met Val Asn Gly Gly Glu Gln Gly Glu Arg Ile Leu His His Ala Ile
130 135 140

Gln Ser Thr Met Ala Gly Lys Gly Val Ser Val Val Val Ile Pro Gly
145 150 155 160

Asp Ile Ala Lys Glu Asp Ala Gly Asp Gly Thr Tyr Ser Asn Ser Thr
165 170 175

Ile Ser Ser Gly Thr Pro Val Val Phe Pro Asp Pro Thr Glu Ala Ala
180 185 190

Ala Leu Val Glu Ala Ile Asn Asn Ala Lys Ser Val Thr Leu Phe Cys

195

200

205

Gly Ala Gly Val Lys Asn Ala Arg Ala Gln Val Leu Glu Leu Ala Glu
 210 215 220

Lys Ile Lys Ser Pro Ile Gly His Ala Leu Gly Gly Lys Gln Tyr Ile
 225 230 235 240

Gln His Glu Asn Pro Phe Glu Val Gly Met Ser Gly Leu Leu Gly Tyr
 245 250 255

Gly Ala Cys Val Asp Ala Ser Asn Glu Ala Asp Leu Leu Ile Leu Leu
 260 265 270

Gly Thr Asp Phe Pro Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala
 275 280 285

Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys
 290 295 300

Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro
 305 310 315 320

His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys
 325 330 335

Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn
 340 345 350

Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu
 355 360 365

Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met
 370 375 380

Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg
 385 390 395 400

Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro

405

410

415

His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala
 420 425 430

Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr
 435 440 445

Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser
 450 455 460

Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu
 465 470 475 480

Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala
 485 490 495

Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu
 500 505 510

Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile
 515 520 525

Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu
 530 535 540

Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly
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Gly Val Gly Ala Met Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile
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Pro Thr Pro

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<212> DNA

<213> Corynebacterium glutamicum

<400> 6

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120

ccggtaccca aaagaaggcc cgccatgagc aggggatatg cgttgatgat ccacaacgct
180

tgggttttcgg tggctgcgag ctgttcacgc agcagaggga gtgcgggtgta gagaatcgag
240

ttgtctacac cgatcagaaa gagaccaccg ctgataacgg cgaggaaagc ccaacgttgg
300

gttttcgtag gcgcttgccg ctgtaagggt tctgaagtca tggatcgtaa ctgtaacgaa
360

tggtcgggtac agttacaact cttttgttgg tgttttagac cacggcgctg tgtggcgatt
420

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<211> 613

<212> DNA

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120

tacggacatc ttatttgcg atccgctgta tctaaccgat catgcagtgc aacgcctgaa
180

cgcgatcccc ggagaaattt ccattggcgt ggattcggtg gagatggcac aggcgacggc
240

gggtttgcgg gaagatatca aggctctgat tgaagtggat tcgggacatc gtagaagtgg
300

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360

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420

tgatgagctt caggctctaa acaacagcgt ccagcgactt gctggcggcc tgacttctgg
480

cggttcctcg ccgtctgccc agtttacaga cgcaatcgat gagatgacgac caggcgtgta
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600

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<210> 11
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<210> 12
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120

agctgttcac gcagcagagg gaggcggtg tagagaatcg agttgtctac accgatcaga
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aagagaccac cgctgataac ggcgaggaaa gcccaacgtt gggttttcgt aggcgcttgc
240

gcctgtaagg tttctgaagt catggatcgt aactgtaacg aatggtcggt acagttacaa
300

ctcttttgtt ggtgttttag accacggcgc tgtgtggcga ttaagacgt cggaaatcgt
360

aggggactgt cagcgtgggt cgggttcttt gaggcgctta gaggcgattc tgtgaggtca
420

ctttttgttg ggtcgggggtc taaatttggc cagttttcga ggcgaccaga caggcgtgcc
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cacgatgttt aaataggcga tcggtgggca tctgtgtttg gtttcgacgg gctgaaacca
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ccattggcgt ggattcggta gagatggcac aggcgacggc gggtttgccg gaagatatca
1080

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1200

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1260

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1320

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20